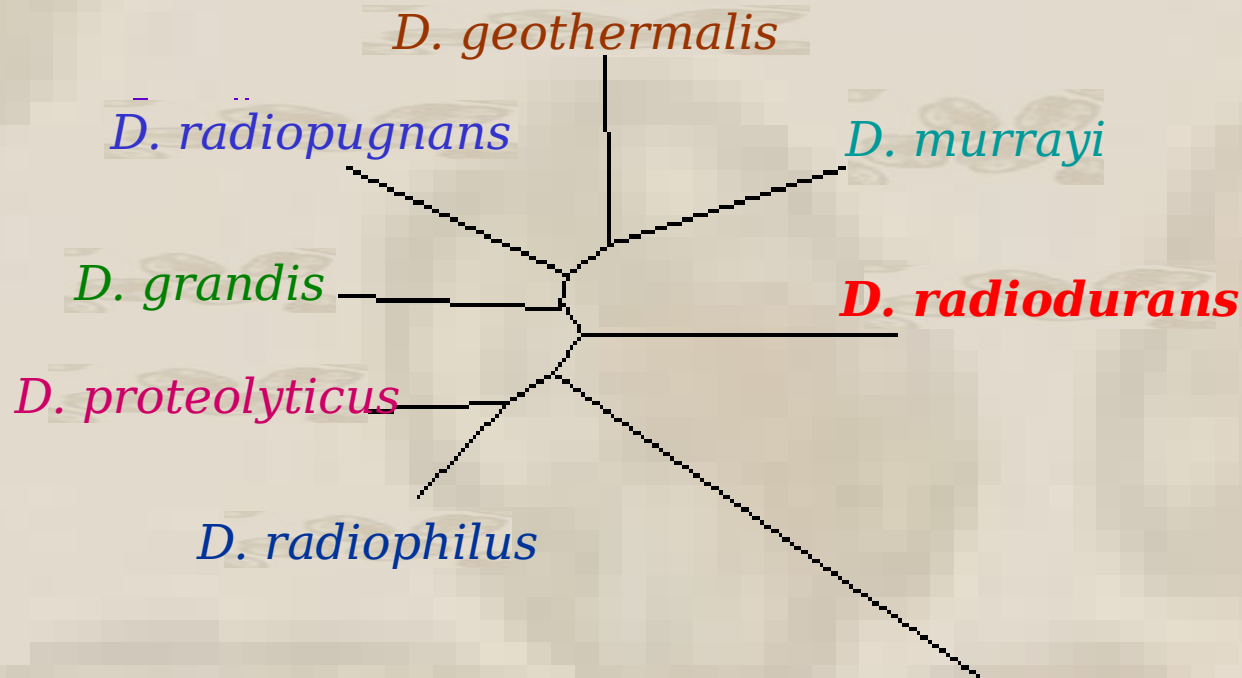
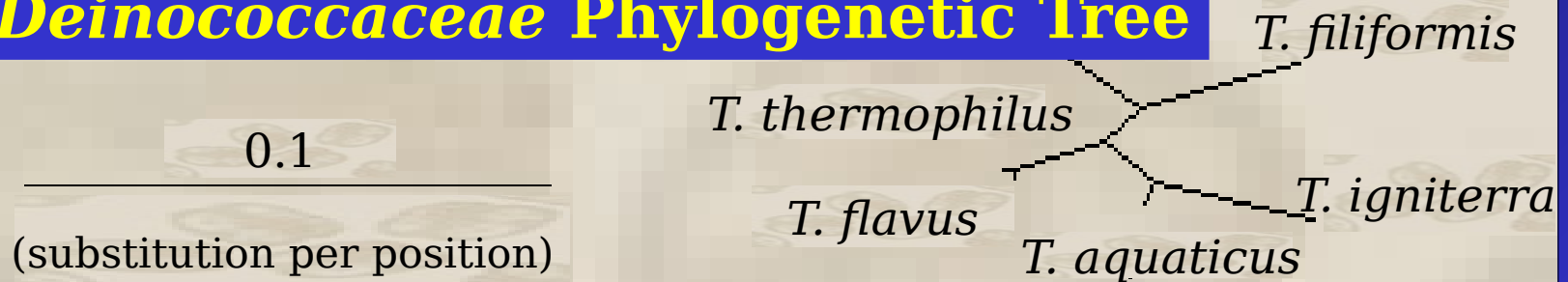


***Deinococcus radiodurans* - a radiation-resistant bacterium**

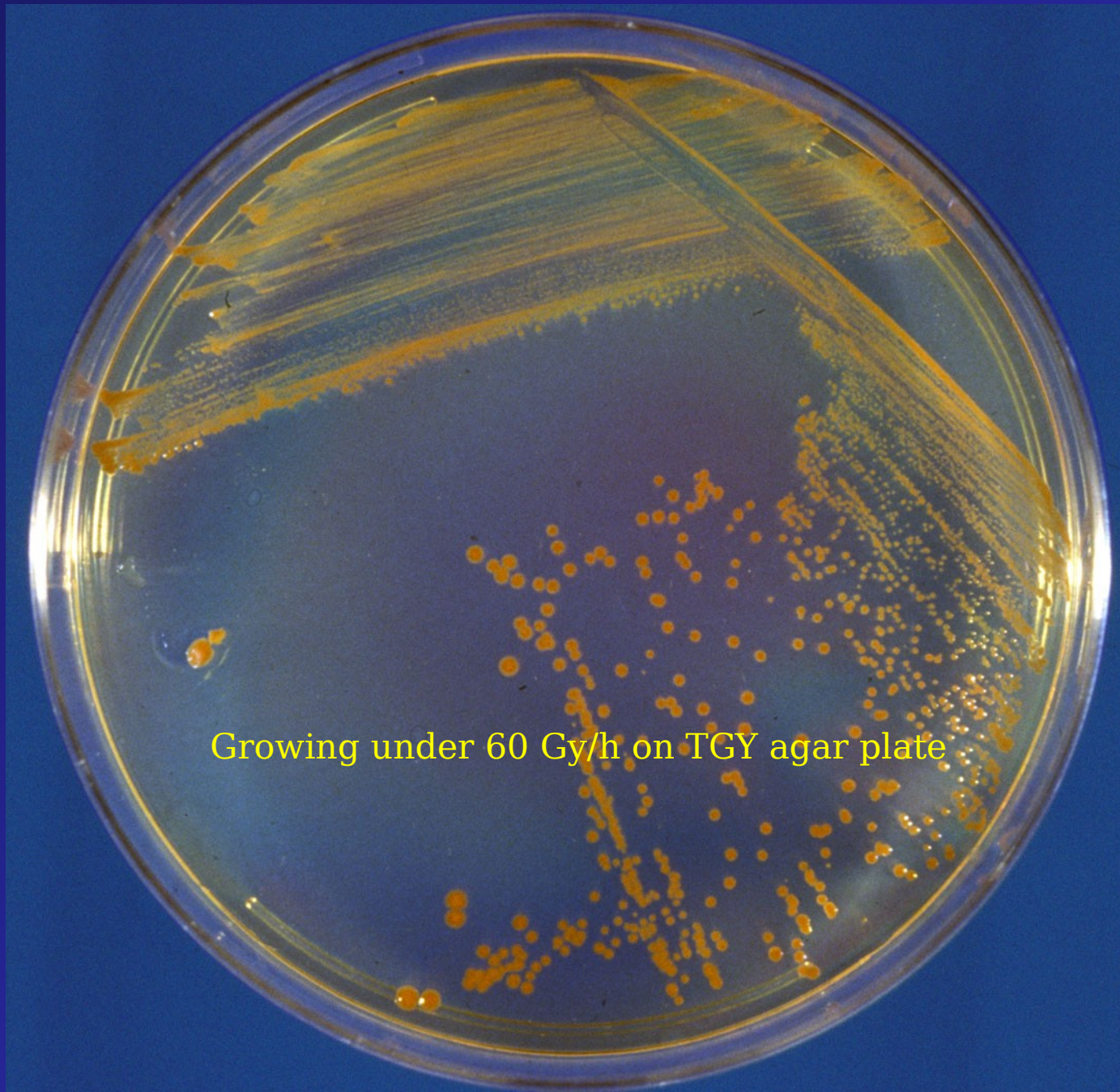


Deinococcaceae Phylogenetic Tree



Neighbor-Joining unrooted phylogenetic tree was built using the PHYLIP program on the rRNA sequences. Five *Thermus* species (*T. thermophilus*, *T. flavus*, *T. aquaticus*, *T. igniterra*) are included as an outgroup. The *Deinococcus/Thermus* group is deeply branched in bacterial trees with putative relationships with the actinobacteria/cyano-bacteria branch. The tree can be found elsewhere (see for example, Wolf et al., BMC Evol. Biol. 2001, Oct 20;1(1):8).

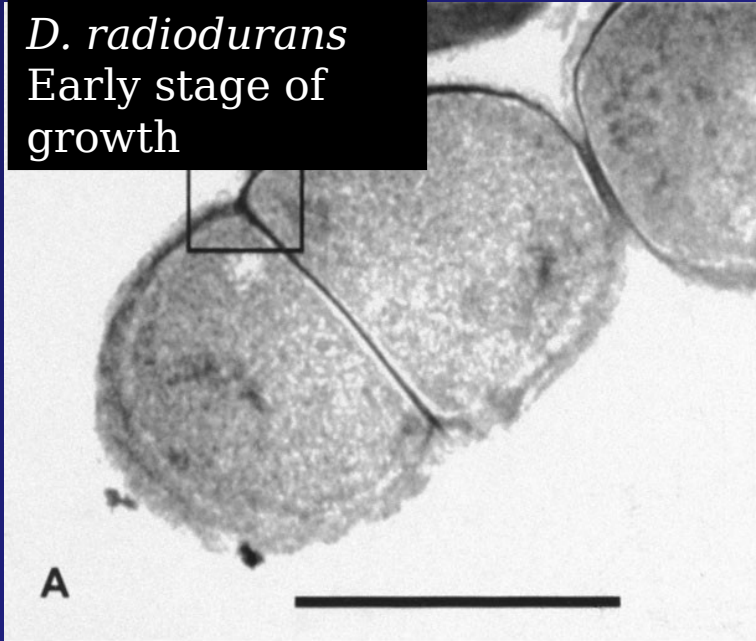
D. radiodurans



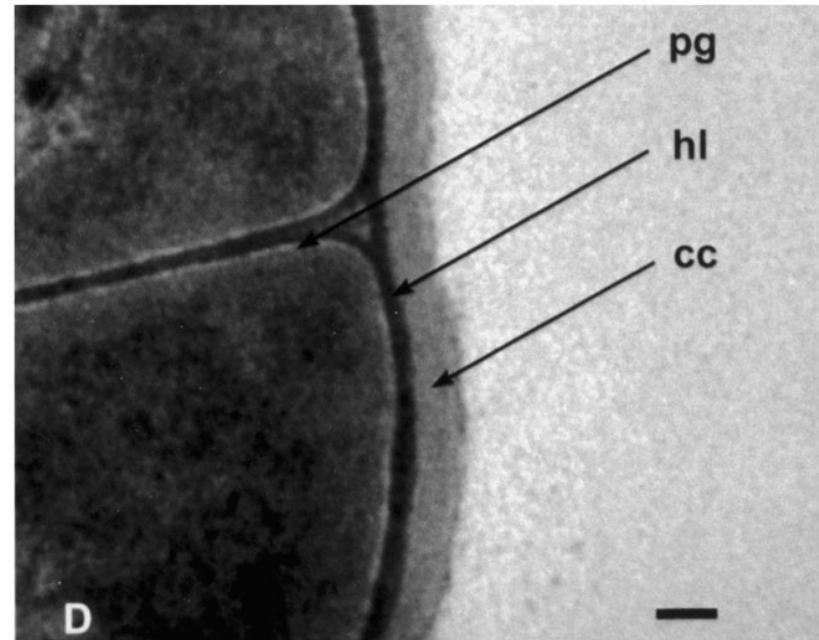
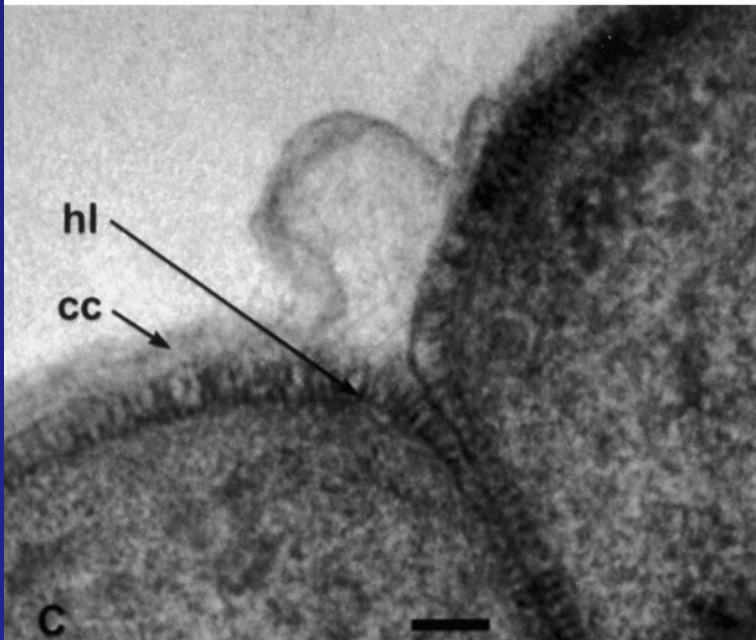
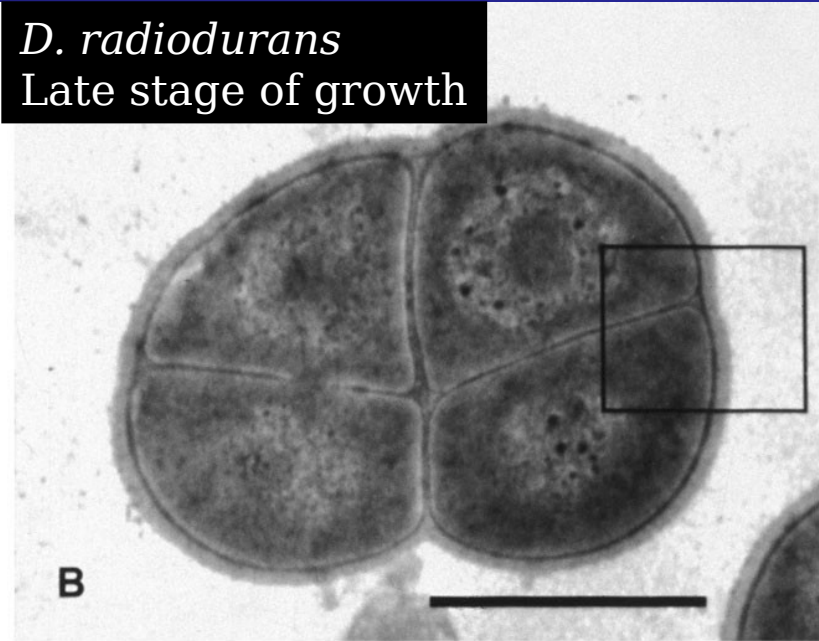
Growing under 60 Gy/h on TGY agar plate

The Structure of *D. radiodurans*

D. radiodurans
Early stage of growth



D. radiodurans
Late stage of growth



D. radiodurans: The Ultimate DNA Assembly Machine

D. radiodurans

1.75M rad, Ohr

0.013 DSB/Gy

With David Schwarz, University of Wisconsin, Madison

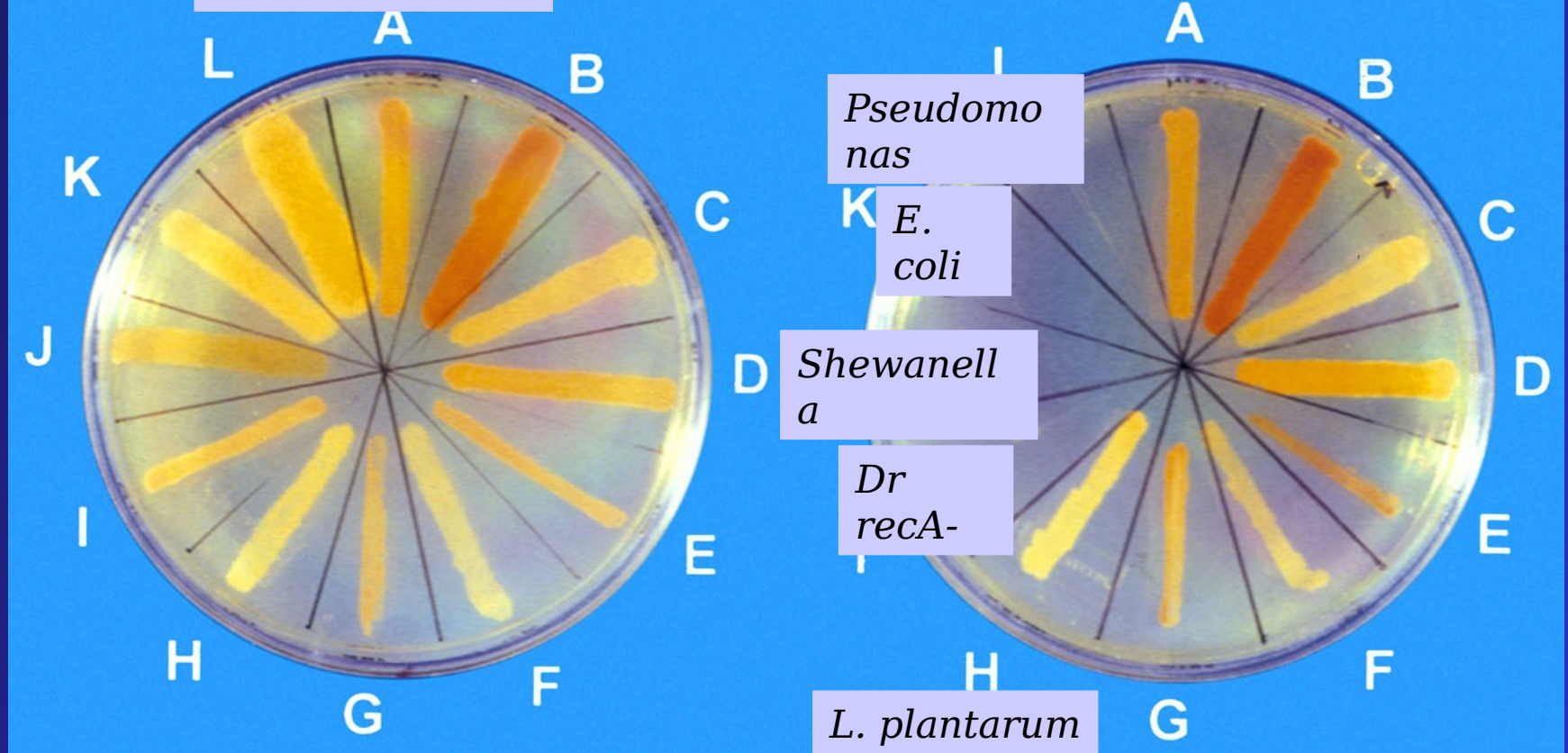
D. radiodurans

1.75M rad, 24hr

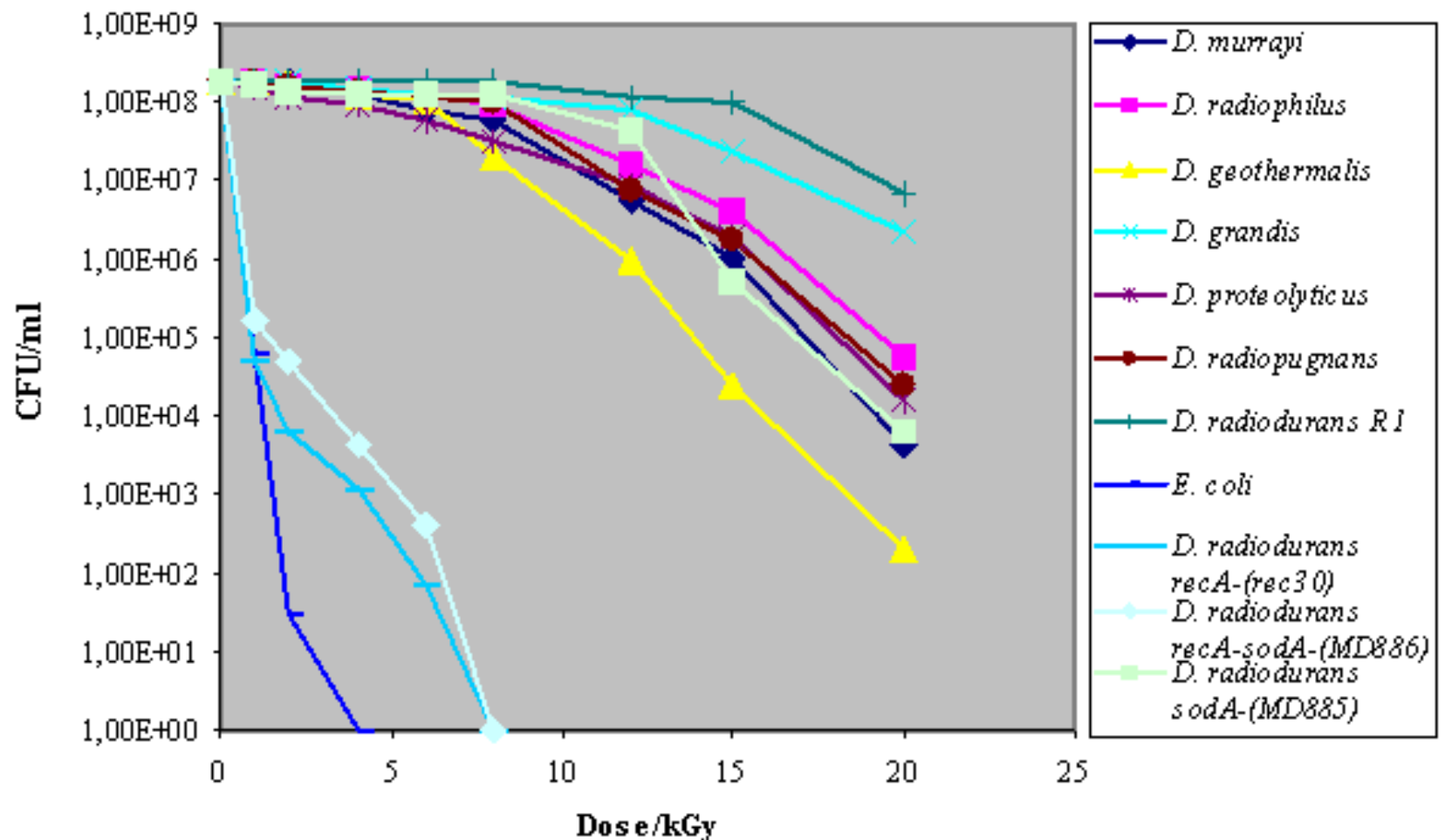
Resistance to Chronic Irradiation

Control rich
medium

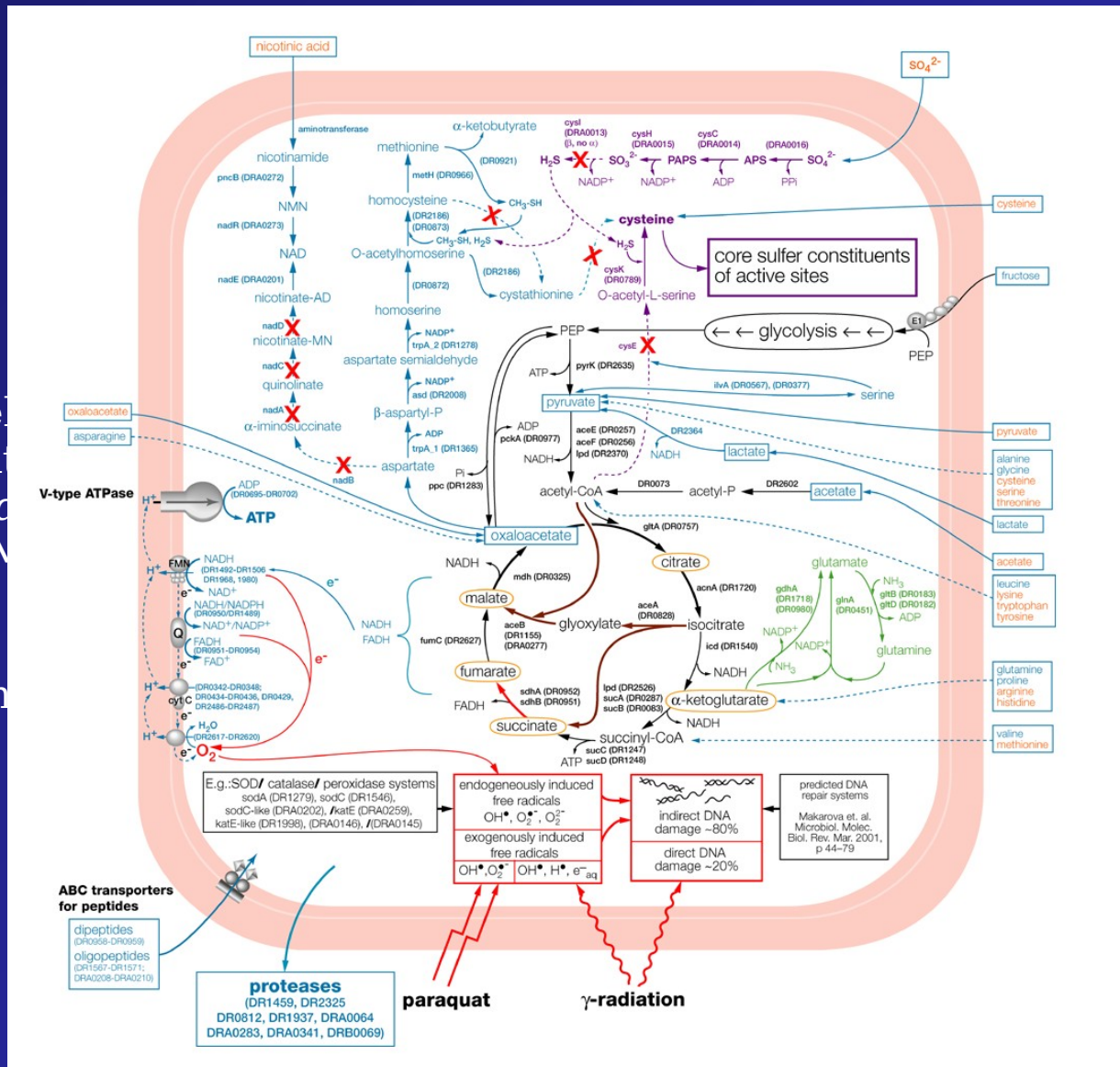
+60 Gy/Hour



Resistance to Acute Irradiation



Predicted *Deinococcus* Metabolic Pathways



Unlike relative radiation sensitive bacteria, *D. radiodurans* recovers on DNA after 10 days of exposure to radiation compared to rich medium.

The lack of a clearly identifiable unique DNA repair system in *D. radiodurans* has given rise to three competing views of the mechanisms responsible for its extraordinary survival

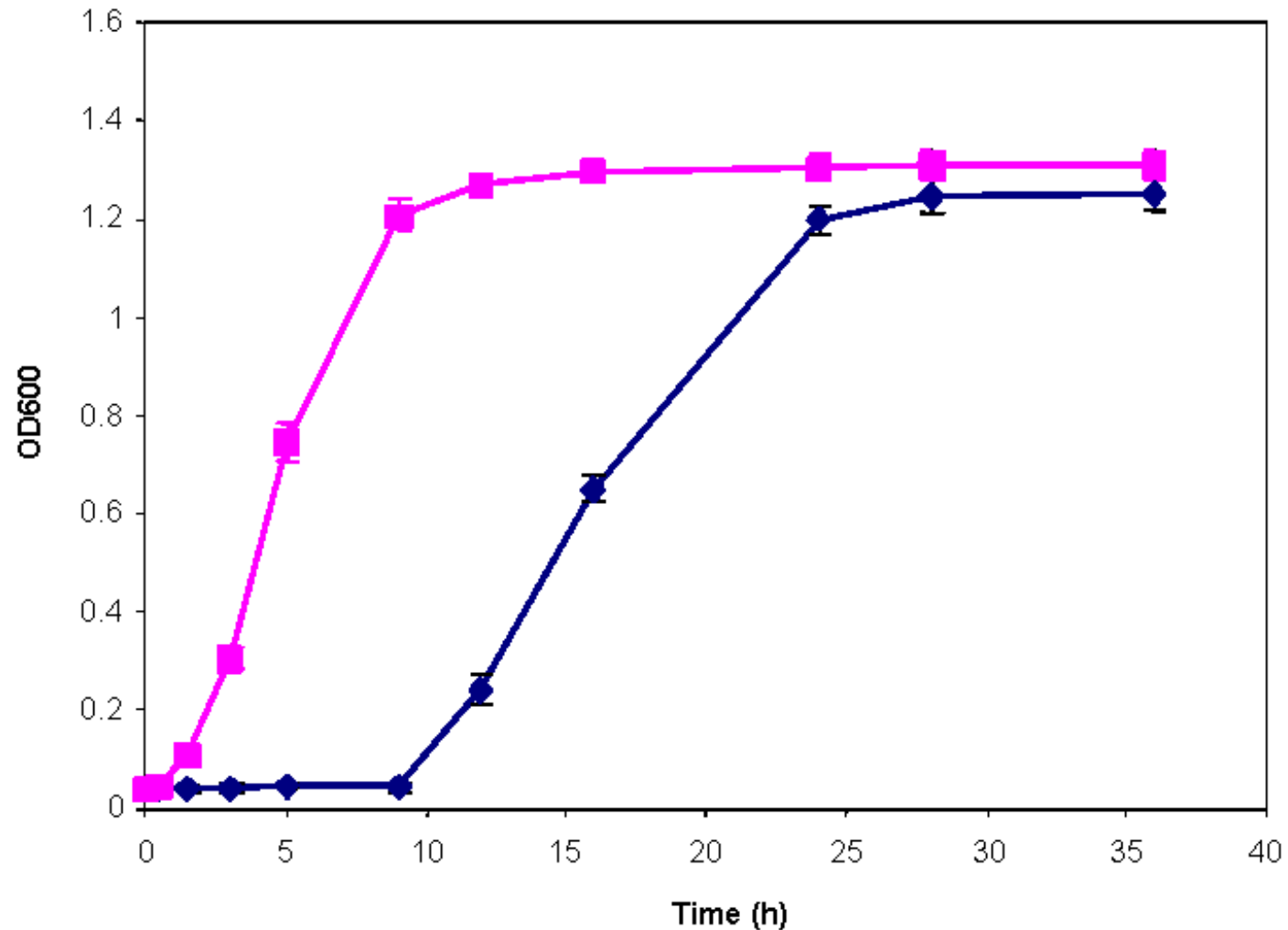
- (i) there are novel repair functions encoded among hypothetical genes predicted by genomic annotation
- (ii) *D. radiodurans* uses conventional DNA repair pathways, but with greater efficiency than other bacteria; or
- (iii) DNA repair in *D. radiodurans* is facilitated by its ringlike chromosomal structures.

The emphasis of these hypotheses is on DNA repair of irradiation-induced damage, with little consideration given to the possibility that protection against DNA-damage during or after irradiation could be key to recovery.

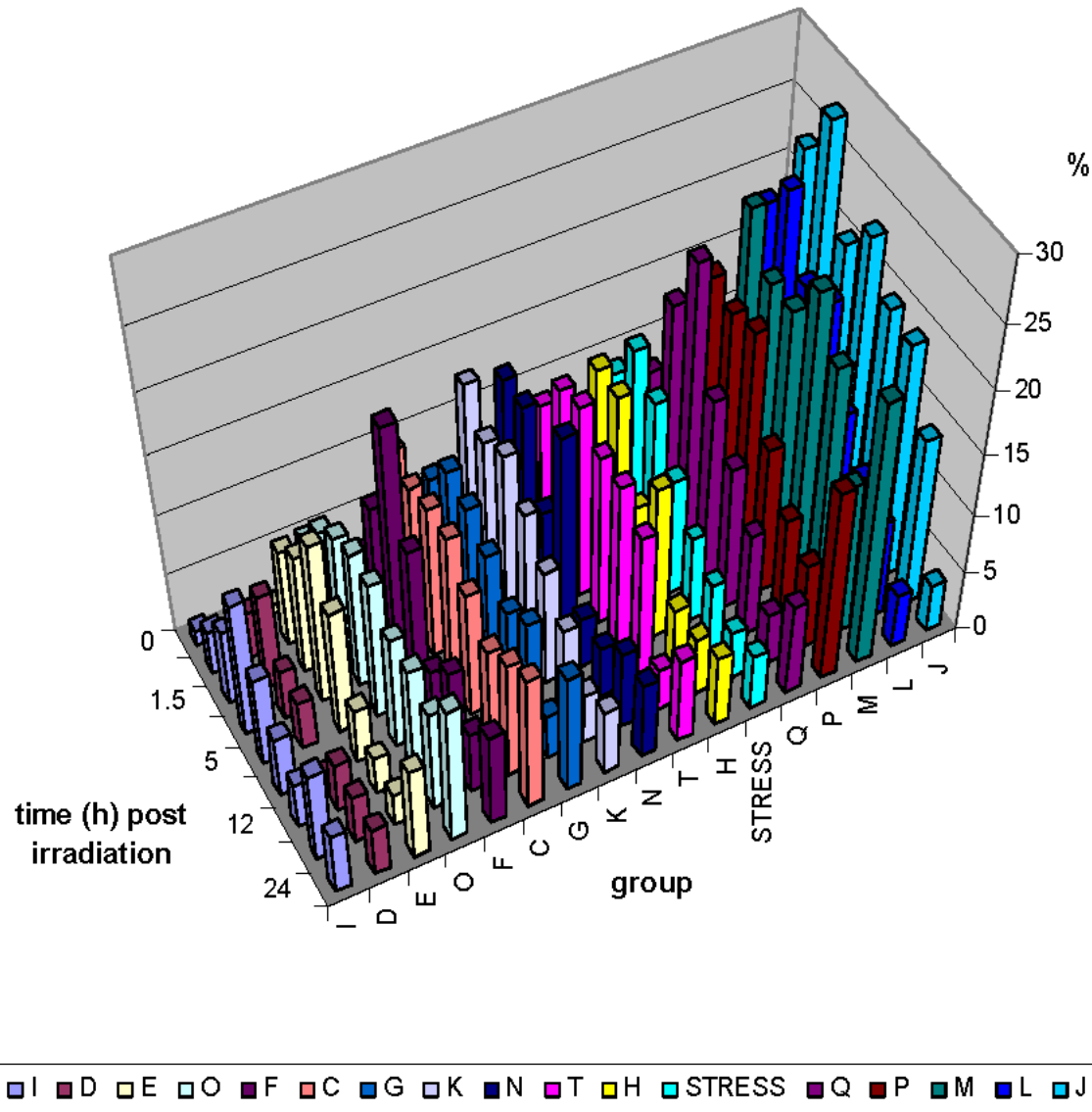
To read how very muddy the field of understanding is, see 'Unlocking radiation resistance mechanisms: still a long way to go.' Issay Narumi, *Trends in Microbiology* September 2003, p. 422-425,. Also, Edwards J.S. & Battista J.R. *Trends in Biotechnology* September 2003,

p. 381-382.

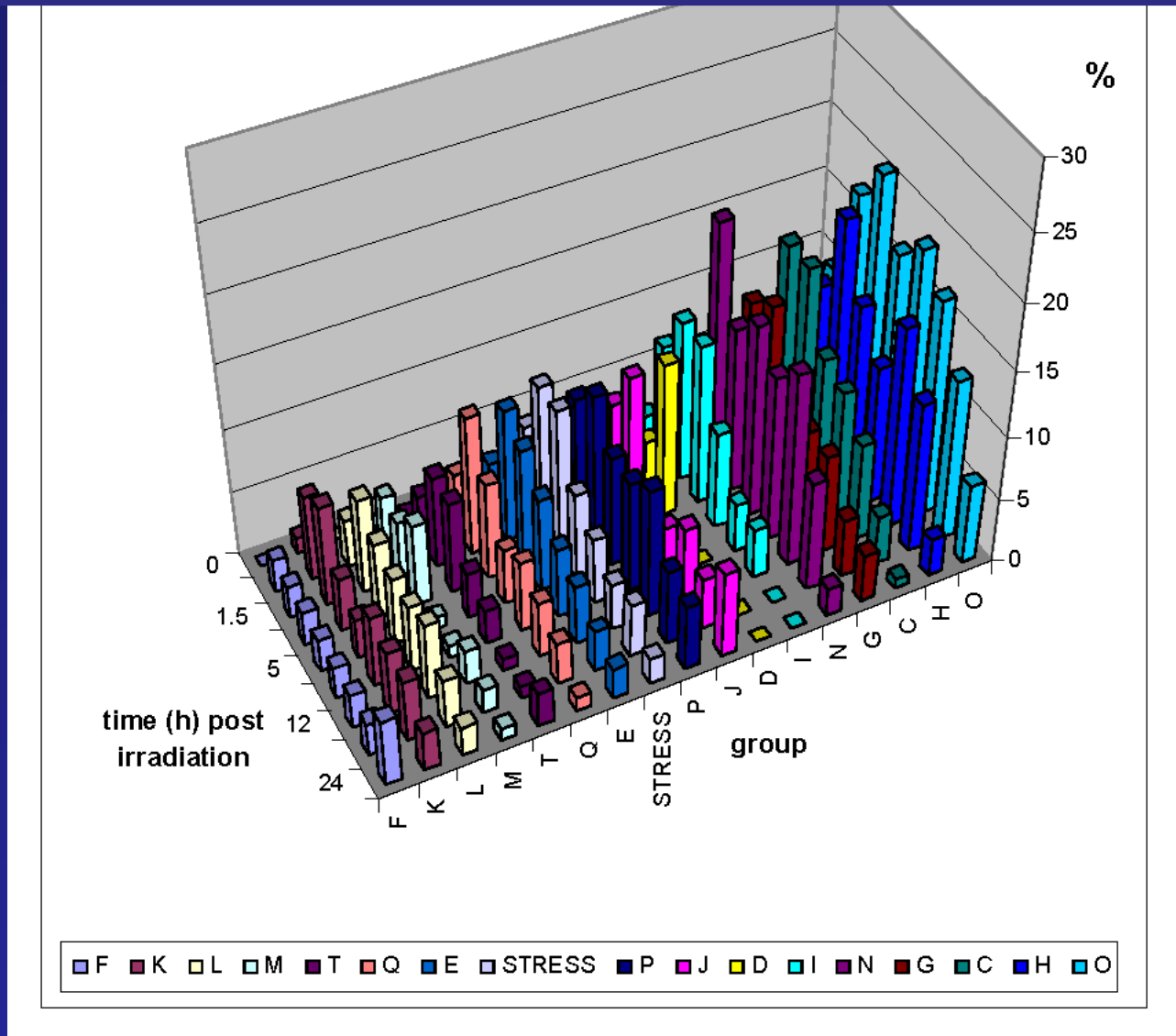
Effect of High-Dose Acute Irradiation on *D. radiodurans* Growth



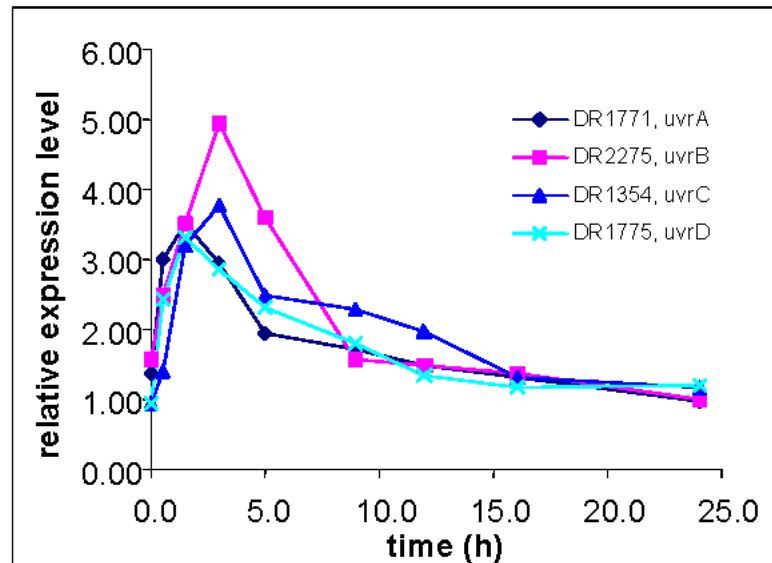
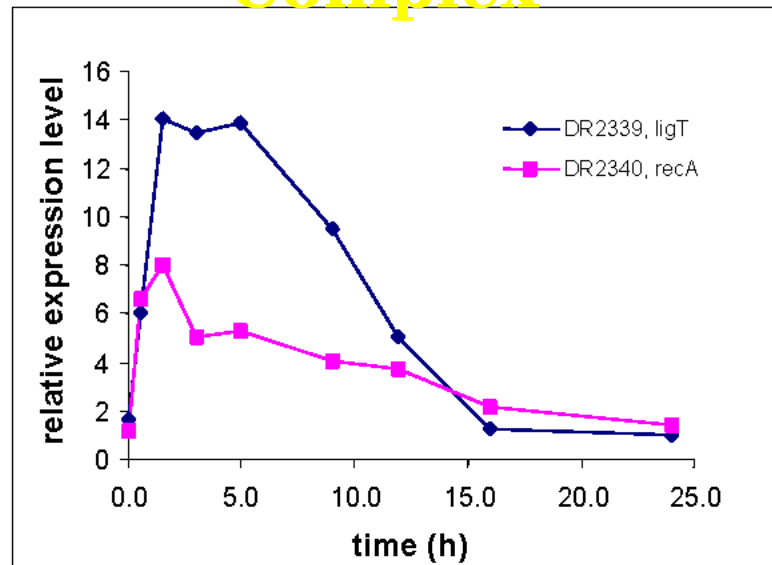
Up-Regulated Genes in Different Functional Gr



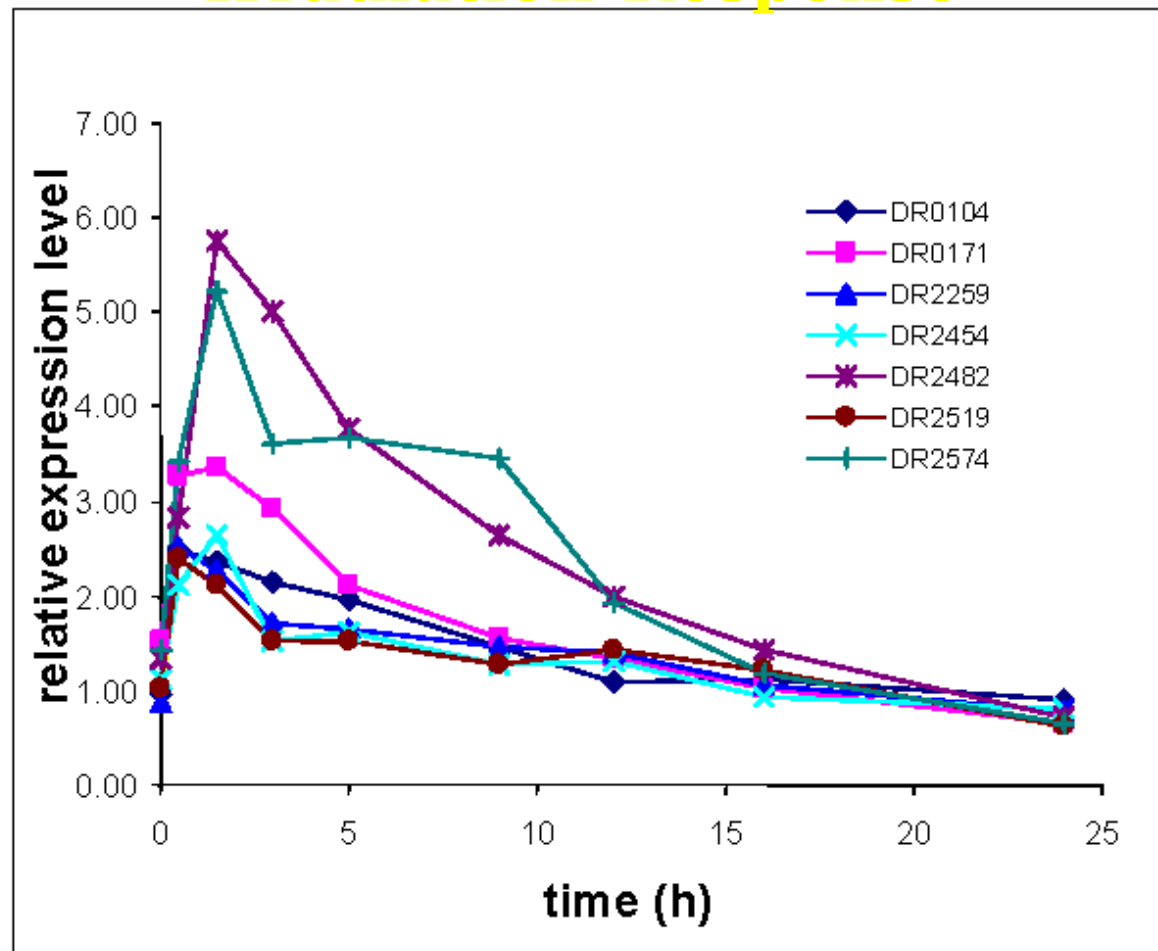
Down-Regulated Genes in Different Functional Groups



Coordinated Expression of Genes Belonging to the Same Operon or Multi-Subunit Complex



Expression Patterns of Predicted Transcriptional Regulators Potentially Involved in the Regulation of *D. radiodurans*' Irradiation-Response



Different Functional Groups of Genes and Operons of *D. radiodurans* with Early-Mid Expression *recA*-like Patterns and the Result of ORF Disruption

(marked in green)

	Gene_ID ^a	Function group ^b	Protein description and comments	Maximum induction level (fold)	Maximum induction time (hr)	Result of ORF disruption
1	DR0003	-	Uncharacterized protein	14	1.5	m resist to 9 kGy
2	DR0050	L	DinB/YfiT family protein	4	3	
3	DR0051	S	Small cysteine-rich protein of the HesB family	6	3	
4	DR0052	-	Uncharacterized conserved protein	7	1.5	
5	DR0053	L	DinB/YfiT family protein	10	3	m resist to 9 kGy
6	DR0070	ST?	Uncharacterized protein	4	9	m sens to 5 kGy, homozyg
7	DR0103	R	Predicted metal-binding protein	6	1.5	
8	DR0105	ST	LEA76 family desiccation resistance protein	3	0.5	m resist to 9 kGy
9	DR0140	-	Uncharacterized protein	6	1.5	m resist to 9 kGy
10	DR0160	-	Conserved membrane protein	4	1.5	
11	DR0161	S	AmsJ/WcaK related protein, possibly involved in exopolysaccharide biosynthesis	8	1.5	
12	DR0203	R	Uncharacterized membrane protein	4	1.5	
13	DR0204	R	Uncharacterized membrane protein	6	3	

Molecular Weight

4325

3850

3375

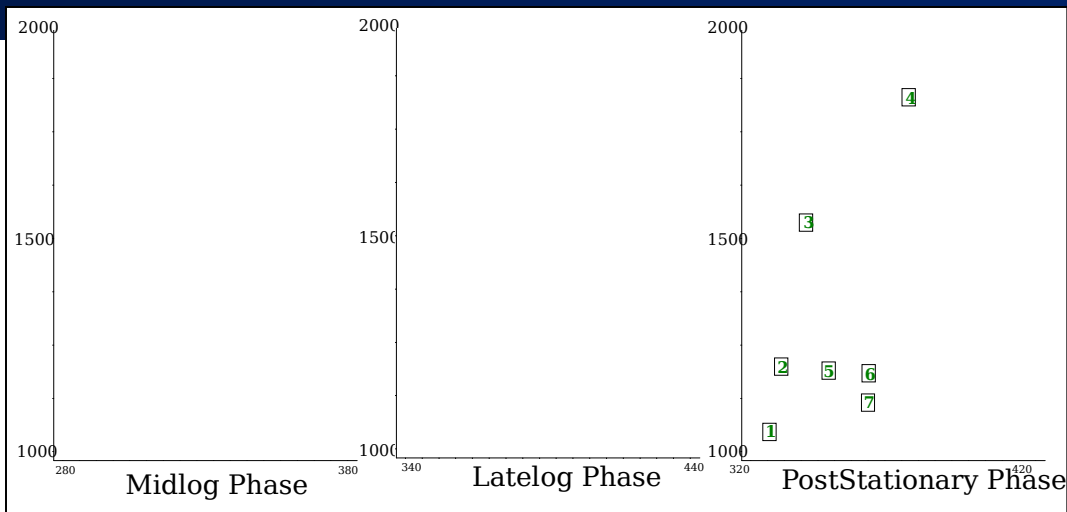
2900

2425

1950

1475

1000



100

200

300

400

500

600

700

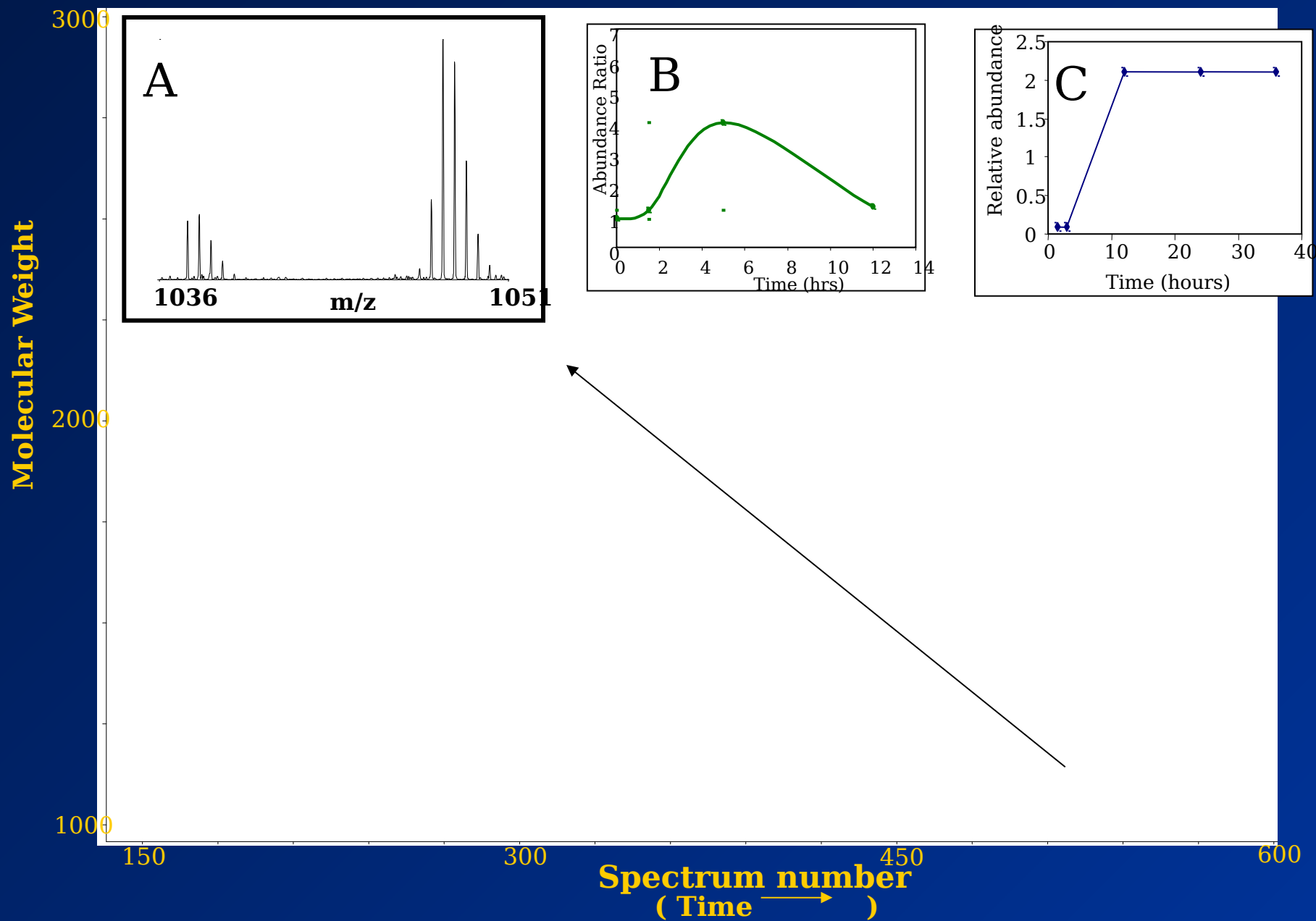
800

Spectrum number
(Time →)

See next slide for comm

2D display of a capillary LC-FTICR analysis in which >50,000 putative polypeptides were detected from a tryptic digest of proteins isolated from *D. radiodurans* harvested in mid log phase. The inset shows three 2-D displays for peptides isolated from *D. radiodurans* harvested in midlog, late log and post stationary phases. Within the inset, spot size has been adjusted to show highly abundant species as larger spots creating a display similar to that of a 2-D PAGE.

Less abundant  More abundant



	A	B	C	D	E	F	G	H	I	J	K	L	M
Amino Acid Biosynthesis													
Cofactor Biosynthesis													
Cell Envelope													
Cellular Processes													
Central Intermediary Metabolism													
Conserved Hypothetical													
DNA Metabolism													
Energy Metabolism													
Fatty Acid and Phospholipid Metabolism													
Hypothetical													
Protein Folding, Modification and Secretion													
Phage Related and Transposon Proteins													
Protein Synthesis													
Nucleotide Synthesis													
Regulatory Functions													
Transcription													
Transport and Binding Proteins													
Unknown													

